

FIG. 1

USE OF ANTIBODIES AGAINST THE MUC18 ANTIGEN

Bar-Eli, et al.

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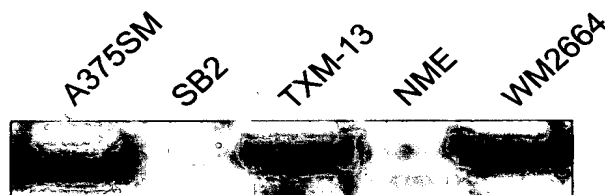


FIG. 2

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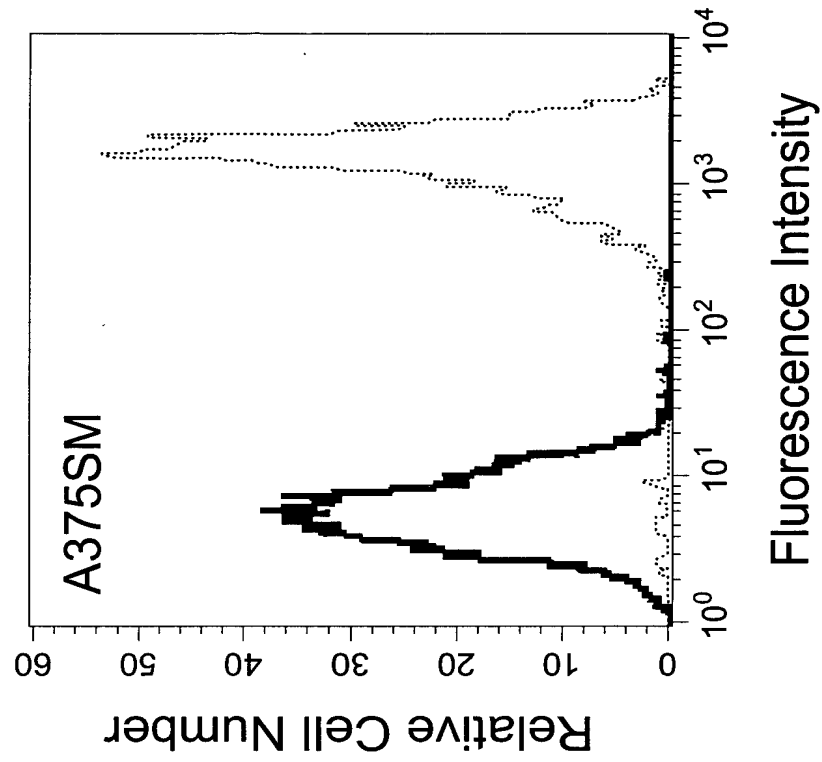


FIG. 3B

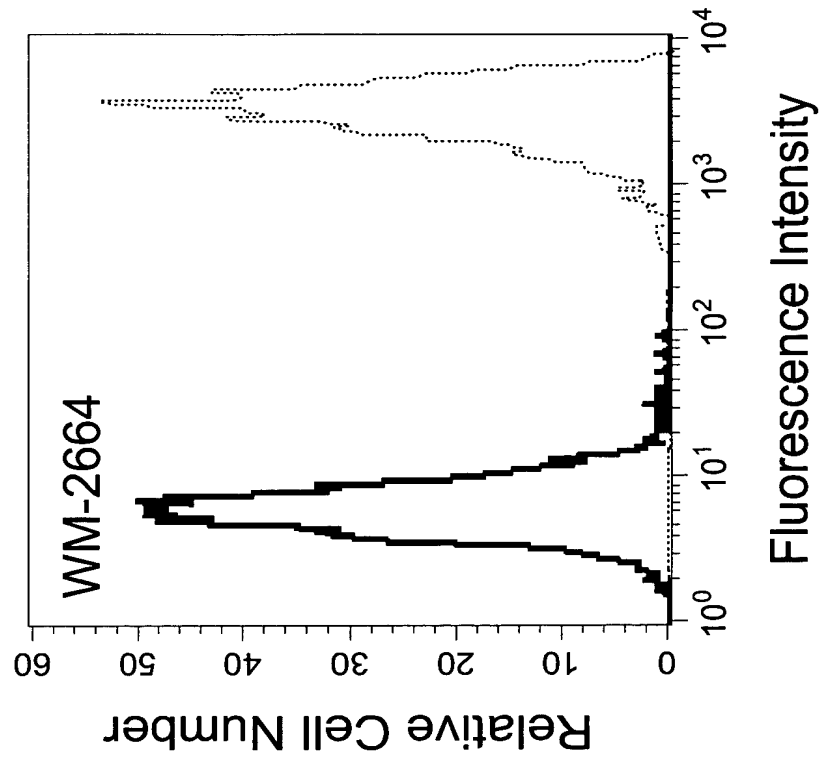


FIG. 3A

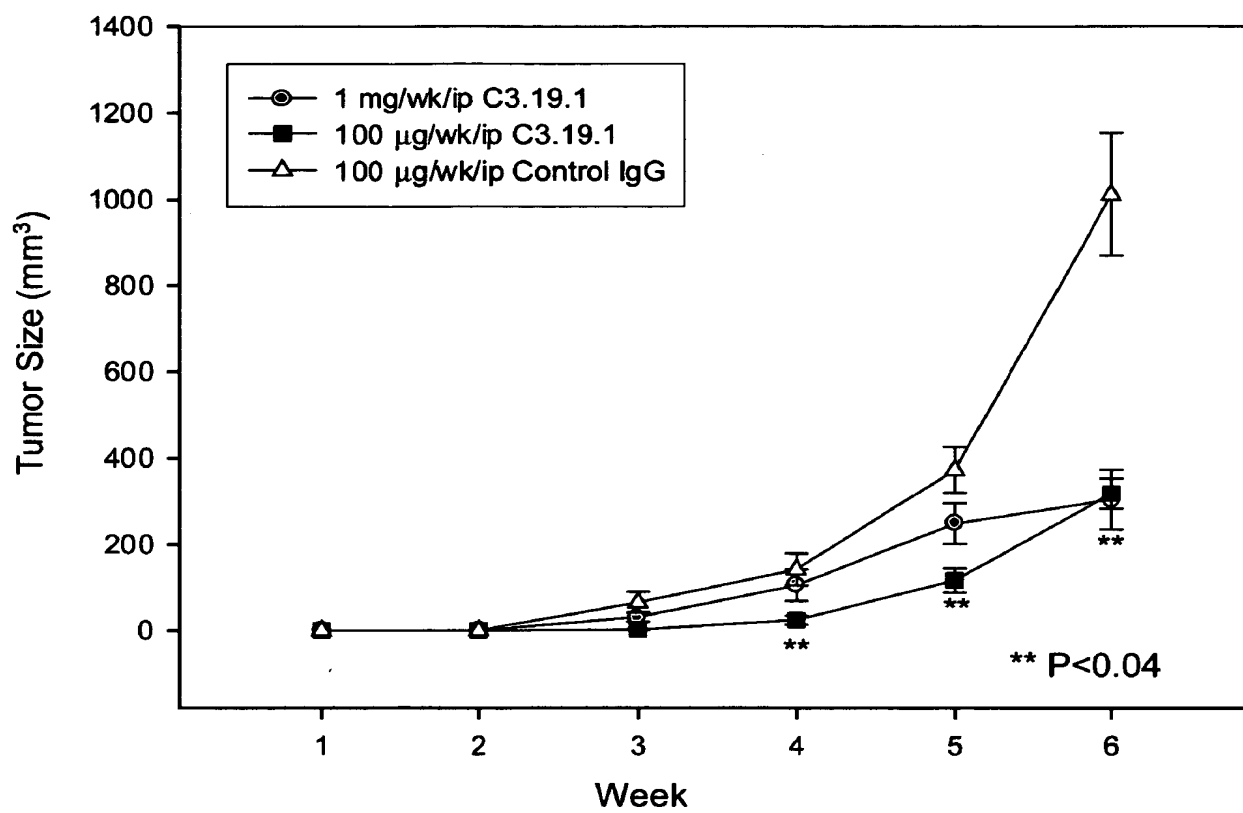


FIG. 4

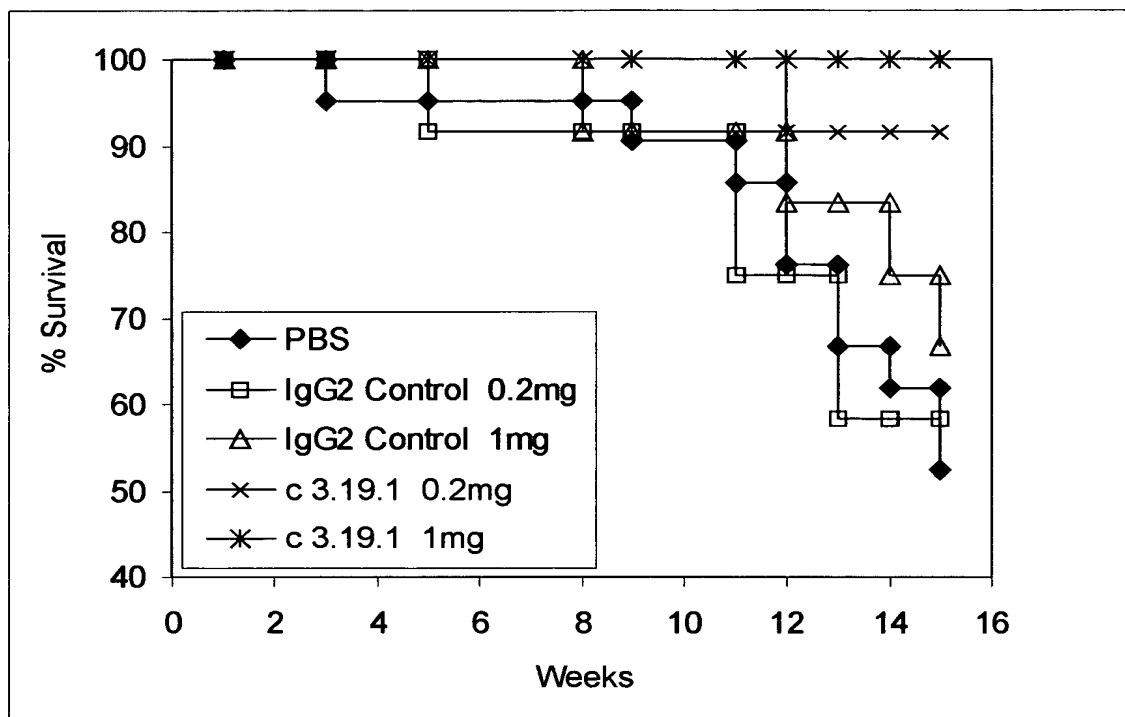


FIG. 5

ANTI-MUC18 ANTIBODY C3.19.1

Nucleotide Sequence of Heavy Chain Variable Region

5' -

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGC
ACTGTCTCTGGTGGCTCCATCAGTAGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGA
CTGGAGTGGATTGGCTATATCTATTACACTTGGACCTCCAACCTACAACCCCTCCCTCAAGAGTCGC
GTCACCATATCAGTGGACACGTCCAAAAACCAGTTCTCCCTGAGGCTGAGTTCTGTGACCGCTGCG
GACACGGCCGTTTATTACTGTGCGAGAGATCAGGGGCAGTGGTTACTACCCGATGCTTTTGATATC
TGGGGCCAAGGGACAATGGTCACCGTCTCTTCAG 3' (SEQ ID NO: 3)

Amino Acid Sequence of Heavy Chain Variable Region

QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYTWTSNYPNPSLKSR
VTISVDTSKNQFSLRLSSVTAADTAVYYCARDQGQWLLPDAFDIWQGQTMVTVSS (SEQ ID NO:1)

Nucleotide Sequence of Light Chain Variable Region

5' -

GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCTCC
TGCAGGTCTAGTCAGAGCCTCCTGCGTAGTAATGGATACAACCTATTTGGATTGGTACCTGCAGAAG
CCAGGACAGTCTCCACATCTCCTGATCTATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGG
TTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTT
GGGGTTTATTACTGCATGCAAGCTCAACAAAGTCCGATCACCTTCGGCCAAGGGACACGACTGGAG
ATTAAAC 3' (SEQ ID NO: 4)

Amino Acid Sequence of Light Chain Variable Region

DIVMTQSPLSLPVTPGEPASISCRSSQSLLRNNGYNYLDWYLQKPGQSPHLLIYLGSNRASGVPDR
FSGSGSGTDFTLKISRVEAEDVGVYYCMQAQQSPITFGQGRLEIK (SEQ ID NO: 2)

FIG. 6

ANTI-MUC18 ANTIBODY C6.11.13

Nucleotide Sequence of Heavy Chain Variable Region

5' -

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGC
ACTGTCTCTGGTGGCTCCATCAGCAGTGGTACTTACCACTGGAGCTGGATCCGCCAGCACCCAGGG
AAGGGCCTGGAGTGGATTGGGTACATCTATTACAGTGGGAGCACCTACTACAACCCGTCCCTCAAG
AGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACT
GCCGCGGACACGGCCGTGTATTACTGTGCGAGAGGGGGAGATGGCTACAAGTACTGGGGCCAGGGA
ACCCTGGTCACCGTCTCCTCAG-3' (SEQ ID NO: 7)

Amino Acid Sequence of Heavy Chain Variable Region

QVQLQESGPGLVKPSQTLSTCTVSGGSISSGTYHWSWIRQHPGKGLEWIGYIYYSGSTYYNPSLK
SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGDGYKYWGQGLTVTVSS (SEQ ID NO: 5)

Nucleotide Sequence of Light Chain Variable Region

5'

GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGGAAAGAGCCACCCTCTCC
TGCAGGGCCAGTCAGAGTGTTAGCAACAACCTTAGCCTGGTATCAGCAGAAACCTGGCCAGGCTCCC
AGGCTCCTCATCTATGGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCACTGGCAGTGGG
TCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGT
CAGCAGTATAATAACTGGCCTCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAAC 3'
(SEQ ID NO: 8)

Amino Acid Sequence of Light Chain Variable Region

EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLLIYGASTRATGIPARFSGSG
SGTEFTLTISSLQSEDFAVYYCQQYNWPRTFGQGTKVEIK (SEQ ID NO: 6)

FIG. 7

ANTI-MUC18 ANTIBODY C3.10

Nucleotide Sequence of Heavy Chain Variable Region

```

1  CAGGTGCAGC  TGCAGGAGTC  GGGCCCAGGA  CTGGTGAAGC  CTTCGGAGAC  CCTGTCCCTC
61  ACCTGCACTG  TCTCTGGTGG  CTCCATCAGT  AGTTACTACT  GGAGCTGGAT  CCGGCAGCCC
121  CCAGGGAAGG  GACTGGAGTG  GATTGGCTAT  ATCTATTACA  CTTGGACCAC  CAACTACAAC
181  CCCTCCCTCA  AGAGTCGCGT  CACCATATCA  GTGGACACGT  CCAAGAACCA  GTTCTCCCTG
241  AGGCTGAGCT  CTGTGACCGC  TGGGACACG  GCCCTTTATT  ACTGTGCGAG  AGATCAGGGG
301  CAGTGGTTAC  TACCCGATGC  TTTTGATATC  TGGGGCCAAG  GGACAATGGT  CACCGTCTCT
361  TCAG (SEQ ID NO: 11)

```

Amino Acid Sequence of Heavy Chain Variable Region

```

1  QVQLQESGPG  LVKPSETLSL  TCTVSGGSIS  SYYSWIRQP  PGKGLEWIGY  IYYTWTNLYN
61  PSLKSRVTIS  VDTSKNQFSL  RLSSVTAADT  ALYYCARDQG  QWLLPDAFDI  WGQGTMTVTVS
121  S (SEQ ID NO: 9)

```

Nucleotide Sequence of Light Chain Variable Region

```

1  GACATCCAGA  TGACCCAGTC  TCCATCCTCC  CTGTCTGCAT  CTGTAGGAGA  CAGAGTCACC
61  ATCACTTGCC  GGGCAAGTCA  GAGCATTAGC  AACTATTTAA  ATTGGTATCA  GCAGAAACCA
121  GGAAAAGCCC  CTAAGCTCCT  GATCTATGGT  GCATCCAGTT  TGCAAAGTGG  GGTCCCATCA
181  AGGTTCAAGT  GCAGTGGATC  TGGGACAGAT  TTTACTCTCA  CCATCAGCAG  TCTGCAACCT
241  GAAGATTTTG  CAACCTACTA  CTGTCGACAG  AGTTACAGTA  CCCCTCCGGA  GTGCAGTTTT
301  GGCCAGGGGA  CCAAGCTGGA  GATCAAAC (SEQ ID NO: 12)

```

Amino Acid Sequence of Light Chain Variable Region

```

1  DIQMTQSPSS  LSASVGDRV  ITCRASQSI  NYLNWYQKP  GKAPKLLIYG  ASSLQSGVPS
61  RFSGSGSGTD  FTLTISSLQ  EDFATYYCR  SYSTPPECS  F GQGTKLEIK (SEQ ID NO:10)

```

FIG. 8

ANTI-MUC18 ANTIBODY C3.22

Nucleotide Sequence of Heavy Chain Variable Region

```
1 CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTACAGAC CCTGTCCCTC
61 ACCTGCACTG TCTCTGGTGG CTCCATCAGC AGTGGTGGTT ACTACTGGAC TTGGATCCGC
121 CAGCACCCAG GGAAGGGCCT GGAGTGGATT GGGTTCATCT ATTACAGTGG GAGCACCTAC
181 TACAACCCGT CCCTCAAGAG TCGAGTTACC ATATCAGTAG ACACGTCTAA GAACCAGTTC
241 TCCCTGAAGC TGAGCTCTGT GACTGCCGCG GACACGGCCG TGTATTACTG TGCAGAGAGAG
301 GGAGATGGCT TTGACTACTG GGGCCAGGGA ACCCTGGTCA CCGTCTCCTC AG
(SEQ ID NO: 15)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
1 QVQLQESGPG LVKPSQTLST TCTVSGGSIS SGGYYWTWIR QHPKGLEWI GFIIYSGSTY
61 YNPSLKSRVT ISVDTSKNQF SLKLSSVTAA DTAIVYICARE GDGFDYWGQG TLVTVSS
(SEQ ID NO: 13)
```

Nucleotide Sequence of Light Chain Variable Region

```
1 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CAGAGTCACC
61 ATCACTTGCC GGGCAAGTCA GGGCATTAGA AATGATTTAG GCTGGTATCA GCAGAAACCA
121 GGGAAAGCCC CTAAGCGCCT GATCTATGCT GCATCCAGTT TGCAAAGTGG GGTCCCATCA
181 AGGTTCAGCG GCAGTGGATC TGGGACAGAA TTTACTCTCA CAATCAGCAG CCTGCAGCCT
241 GAAGATTTTG CAACTTATTA CTGTCTACAG CATAATAGTT ACCCGCTCAC TTTCGGCGGA
301 GGGACCAAGG TGGAGATCAA AC (SEQ ID NO: 16)
```

Amino Acid Sequence of Light Chain Variable Region

```
1 DIQMTQSPSS LSASVGDRVT ITCRASQGIR NDLGWYQQKP GKAPKRLIYA ASSLQSGVPS
61 RFSGSGSGTE FTLTISSLQP EDFATYYCLQ HNSYPLTFGG GTKVEIK (SEQ ID NO: 14)
```

FIG. 9

ANTI-MUC18 ANTIBODY C3.27

Nucleotide Sequence of Heavy Chain Variable Region

```
1 CAGGTGCAGC TGCAGGAGTC GGGCCCAGGA CTGGTGAAGC CTTCCGAGAC CCTGTCCCTC
61 ACCTGCACTG TCTCTGGTGG CTCCATCAGT AGTTACTACT GGAGCTGGAT CCGGCAGCCC
121 CCAGGGAAGG GACTGGAGTG GATTGGCTAT ATCTATTACA CTTGGACCTC CAACTACAAC
181 CCCTCCCTCA AGAGTCGCGT CACCATATCA GTGGACACGT CCAAGAACCA GTTCTCCCTG
241 AGGCTGAGTT CTGTGACCGC TGC GGACACG GCCGTTTACT ACTGTGCGAG AGATCAGGGG
301 CAGTGGTTAC TACCCGATGC TTTTGATATC TGGGGCCAAG GGACAATGGT CACCGTCTCT
361 TCAG (SEQ ID NO: 19)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
1 QVQLQESGPG LVKPSSETLSL TCTVSGGSIS SYVSWIRQP PGKGLEWIGY IYYTWSNRYN
61 PSLKSRVTIS VDTSKNQFSL RLSSVTAADT AVYYCARDQG QWLLPDAFDI WGQGTMTVTS
121 S (SEQ ID NO: 17)
```

Nucleotide Sequence of Light Chain Variable Region

```
1 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CAGAGTCACC
61 ATCACTTGCC GGGCAAGTCA GGGCATTAGA AATGATTTAG GCTGGTATCA GCAGAAACCA
121 GGGAAAGCCC CTAAGCGCCT GATCTATGCT GCATCCAGTT TGCAAAGTGG GGTCCCATCA
181 AGGTTCAGCG GCAGTGGATC TGGGACAGAG TTTACTCTCA CAATCAGCAG CCTGCAGCCT
241 GAAGATTTTG CAACTTATTA CTGTCTACAG CATAATAGTT ACCCGTGGAC GTTCGGCCAA
301 GGGACCAAGG TGGAAATCAA AC (SEQ ID NO: 20)
```

Amino Acid Sequence of Light Chain Variable Region

```
1 DIQMTQSPSS LSASVGDRVT ITCRASQGIR NDLGWYQQKP GKAPKRLIYA ASSLQSGVPS
61 RFSGSGSGTE FTLTISSLQP EDFATYYCLQ HNSYPWTFGQ GTKVEIK
(SEQ ID NO: 18)
```

FIG. 10

ANTI-MUC18 ANTIBODY C3.45

Nucleotide Sequence of Heavy Chain Variable Region

```

1  CAGGTTTCAGC TGGTGCAAGT GGGAGCTGAG GTGAAGAAGC CTGGGGCCTC AGTGAAGGTC
61 TCCTGCAAGG CTTCTGGTTA CACCTTTTTT AGCTATGGTT TCAGCTGGGT GCGACAGGCC
121 CCTGGACAAG GGCTTGAGTG GCTGGGATGG ATCAGCGCTT ACAATGGTAA CACAACTAT
181 GCACAGAAGC TCCAGGGCAG AGTCACCATG ACCACAGACA CTTCCACGAG CACAGCCTAC
241 ATGGAGCTGA GGAGCCTGAG ATCTGACGAC ACGGCCGTGT ATTACTGTGC GAGAGAACT
301 AAGGTTTCGGG GAGTCCACTA CTACGGTATG GACGTCTGGG GCCAAGGGAC CACGGTCACC
361 GTCTCCTCAG (SEQ ID NO: 23)

```

Amino Acid Sequence of Heavy Chain Variable Region

```

1  QVQLVQSGAE VKKPGASVKV SCKASGYTFF SYGFSWVRQA PGQGLEWLGW ISAYNGNTNY
61 AQKLQGRVTM TDTSTSTAY MELRSLRSD TAVYYCARET KVRGVHYYGM DVWGQGTQVT
121 VSS (SEQ ID NO: 21)

```

Nucleotide Sequence of Light Chain Variable Region

```

1  DIVMTQSPDS LAVSLGERAT IICKSSQSIL YSSNNKNYLG WYQQKPGQPP KLLIYWASTR
61 ESGVPARFSG SGSGTDFTLT INSLOAEDVA VYYCQQYYST PRSFGQGTMTV EIK (SEQ ID
NO: 24)

```

Amino Acid Sequence of Light Chain Variable Region

```

1  GACATCGTGA TGACCCAGTC TCCAGACTCC CTGGCTGTGT CTCTGGGCGA GAGGGCCACC
61 ATCATCTGCA AGTCCAGCCA GAGTATTTTA TACAGCTCCA ACAATAAGAA CTAATTAGGT
121 TGGTACCAGC AGAAACCAGG ACAGCCTCCT AAGCTGCTCA TTTACTGGGC ATCTACCCGG
181 GAATCCGGGG TCCCTGCCCC ATTCAGTGGC AGCGGGTCTG GGACAGATTT CACTCTCACC
241 ATCAACAGCC TGCAGGCTGA AGATGTGGCA GTTTATTACT GTCAGCAATA TTATAGTACT
301 CCTCGGTCGT TCGGCCAAGG GACCATGGTG GAAATCAAAC (SEQ ID NO 22)

```

FIG. 11

ANTI-MUC18 ANTIBODY C3.65

Nucleotide Sequence of Heavy Chain Variable Region

```

1  CAGGTGCAGC  TGCAGGAGTC  GGGCCCAGGA  CTGGTGAAGC  CTTACAGAC  CCTGTCCCTC
61  ACCTGCACTG  TCTCTGGTGG  CTCCATCAAC  AGTGGTGGTT  GCTACTGGAG  CTGGATCCGC
121  CAGCACCCAG  GGAAGGGCCT  GGAGTGGATT  GGGTACATCT  ATTCCAGTGG  GAGCACCTAC
181  TACAACCCGT  CCCTCAAGAG  TCGAATTACC  TTATCAGTAG  ACACGTCTAA  GAACCAGTTC
241  TCCCTGAAGC  TGAAGTCTAT  GACTGCCGCG  GACACGGCCG  TGTATTACTG  TGCAGAGAGT
301  CGGGAAACAG  CTGGTTTGA  CTAAGTGGGC  CAGGGAACCC  TGGTCACCGT  CTCCTCAG
(SEQ ID NO: 27)

```

Amino Acid Sequence of Heavy Chain Variable Region

```

1  QVQLQESGPG  LVKPSQTLST  TCTVSGGSIN  SGGCYWSWIR  QHPGKGLEWI  GYIYSSGSTY
61  YNPSLKSRLT  LSVDTSKNQF  SLKLNSMTAA  DTAVYYCARD  RETAGFDYWG  QGTLVTVSS
(SEQ ID NO: 25)

```

Nucleotide Sequence of Light Chain Variable Region

```

1  GACATCCAGA  TGACCCAGTC  TCCATCCTCC  CTGTCTGCAT  CTGTAGGAGA  CAGAGTCACC
61  ATCACTTGCC  AGGCGAGTCA  GGACATTAAC  AACTATTTAA  ATTGGTATCA  GCAGAAACCA
121  GGGAAAGCCC  CTAAGCTCCT  GATCTACGAT  GCATCCAATT  TGGAAACAGG  GGTCCCATCA
181  AGGTTCAGTG  GAAGTGGATC  TGGGACAGAT  TTTACTTTCA  CCATCAGCGG  CCTGCAGCCT
241  GAGGATATTG  CAACATATTA  CTGTCAACAG  TATGATACTC  TCCCTCTCAC  TTTCGGCGGC
301  GGGACCAAGG  TGGAGATCAA  AC (SEQ ID NO: 28)

```

Amino Acid Sequence of Light Chain Variable Region

```

1  DIQMTQSPSS  LSASVGDRVT  ITCQASQDIN  NYLNWYQQKP  GKAPKLLIYD  ASNLETGVPS
61  RFSGSGSGTD  FTFTISGLQP  EDIATYYCQQ  YDTLPLTFGG  GTKVEIK (SEQ ID NO: 26)

```

FIG. 12

ANTI-MUC18 ANTIBODY C6.1

Nucleotide Sequence of Heavy Chain Variable Region

```
1 CAGGTGCAGC TGGTGGAGTC GGGGGGAGGC GTGGTCCAGC CTGGGAGGTC CCTGAGACTC
61 TCCTGTGCAG CCTCTGGATT CACCTTCAGT AGCTATGCCA TGCACTGGGT CCGCCAGGCT
121 CCAGGCAAGG GGCTGGAGTG GGTGGCAGTT ATATCATATG ATGGAAGTAA TAAATACTAT
181 GCAGACTCCG TGAAGGGCCG ATTCACCATC TCCAGAGACA ATTCCAAGAA CACGCTGTAT
241 CTGCAAATGA ACAGCCTGAG AGCTGAGGAC ACGGCTGTGT ATTACTGTGC GAGATCGATT
301 TTTGGAGTGG TTATCGACTA CGGTATGGAC GTCTGGGGCC AAGGGACCAC GGTCACCGTC
361 TCCTCAG (SEQ ID NO: 31)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
1 QVQLVESGGG VVQPGRSLRL SCAASGFTFS SYAMHWVRQA PGKGLEWVAV ISYDGSNKYY
61 ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARSI FGVVIDYGMD VWGQGTTVTV
121 SS (SEQ ID NO: 29)
```

Nucleotide Sequence of Light Chain Variable Region

```
1 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT CTGTAGGAGA CAGAGTCACC
61 ATCACTTGCC GGGCGAGTCA GGGCATTAGA AATTATTTAG CCTGGTATCA GCAGAATCCA
121 GGGAAAGTTC CTAAGCTCCT GATCTATGGT GCATCCACTT TGCAATCAGG GGTCCCATCT
181 CGGTTCAGTG GCAGTGGATC TGGGACAGAT TTTACTCTCA CCATCAGCAG CCTGCAGCCT
241 GAAGATGTTG CAACTTATTA CTGTCAAAG TTTAGCAGTC CCCCATTAC TTTCCGCCCT
301 GGGACCAAAG TGGATATCAG TC (SEQ ID NO: 32)
```

Amino Acid Sequence of Light Chain Variable Region

```
1 DIQMTQSPSS LSASVGDRVT ITCRASQGIR NYLAWYQQNP GKVPKLLIYG ASTLQSGVPS
61 RFSGSGSGTD FTLTISSLQP EDVATYYCQK FSSPPFTFGP GTKVDIS (SEQ ID NO: 30)
```

FIG. 13

ANTI-MUC18 ANTIBODY C6.9

Nucleotide Sequence of Heavy Chain Variable Region

```
1 CAGGTGCAGC TGGAGCAGTC GGGGCCAGGA CTGGTGAAGC CTTCAGAGAC CCTGTCCCTC
61 ACCTGCACTG TCTCTGGTGG CTCCATCAGC AGTGGTACTT ACCACTGGAG CTGGATCCGC
121 CAGCACCCAG GGAGGGGCCT GGAGTGGATT GGATACATCT ATTACAGTGG GAGCACCTAC
181 CACAACCCGT CCCTCAAGAG TCGAATTACC ATATCAGTAG ACACGTCTAA GAACCAGTTC
241 TCCCTGAAGC TGAGCTCTGT GACGGCCGCG GACACGGCCG TGTATTACTG TGCGAGAGGG
301 GGAGATGGCT ACAGATACTG GGGCCAGGGA ACCCTGGTCA CCGTCTCCTC AG
(SEQ ID NO: 35)
```

Amino Acid Sequence of Heavy Chain Variable Region

```
1 QVQLEQSGPG LVKPSETLSL TCTVSGGSIS SGTYHWSWIR QHPGRGLEWI GYIYYSGSTY
61 HNPSLKSRIT ISVDTSKNQF SLKLSSVTAA DTA VYYCARG GDGYRYWGQG TLVTVSS
(SEQ ID NO: 33)
```

Nucleotide Sequence of Light Chain Variable Region

```
1 GAAATAGTGA TGACGCAGTC TCCAGCCACC CTGTCTGTGT CTCCAGGGGA AAGAGCCACC
61 CTCTCCTGCA GGGCCAGTCA GAGTATTAGC AACAACTTCG CCTGGTACCA GCAGAAACCT
121 GGCCAGGCTC CCAGGCTCCT CATCTTTGGT GCATCCACCA GGGCCACTGG TATCCCAGCC
181 AGGTTCAGTG GCAGTGGGTC TGGGACAGAA TTTACTCTCA CCATCAGCAG CCTACAGTCT
241 GAAGATTTTG CAGTTTATTA CTGTCAGCAG TATAATAACT GGCCTCGGAC GTTCGGCCAA
301 GGGACCAAGG TGGAAATCAA AC (SEQ ID NO: 36)
```

Amino Acid Sequence of Light Chain Variable Region

```
1 EIVMTQSPAT LSVSPGERAT LSCRASQSIG NNFAWYQQKP GQAPRLLIFG ASTRATGIPA
61 RFSGSGSGTE FTLTISSLQS EDFAVYYCQQ YNNWPRTFGQ GTKVEIK (SEQ ID NO: 34)
```

FIG. 14

ANTI-MUC18 ANTIBODY C6.2

Nucleotide Sequence of Heavy Chain Variable Region

```

1  CAGGTGCAGC  TGCAGGAGTC  GGGCCCAGGA  CTGGTGAAGC  CCTCGGAGAC  CCTGTCCCTC
61  ACCTGCACTG  TCTCTGGTGG  CTCCATCAGT  ACTTACTACT  GGAGTTGGAT  CCGGCAGCCC
121  CCAGGGAAGG  GACTGGAGTG  GATTGGATAC  ATCTATTACA  CTGGGAACAC  CTAACAAC
181  CCCTCCCTCA  AGAGTCGAGT  CACCGTTTCA  GTTGACACGT  CCAAGAACCA  GTTCTCCCTG
241  AAGCTGAACT  CTGTGACCGC  TGCAGGACAG  GCCGTGTATT  ACTGTGCGAG  AGATCCAGGC
301  CAGTGGCTGG  TCCCTGATGC  TTTTGATATC  TGGGGCCAAG  GGACAATGGT  CTCCGTCTCT
361  TCAG (SEQ ID NO: 39)

```

Amino Acid Sequence of Heavy Chain Variable Region

```

1  QVQLQESGPG  LVKPSETLSL  TCTVSGGSIS  TYYWSWIRQP  PGKGLEWIGY  IYYTGNTYYN
61  PSLKSRVTVS  VDTSKNQFSL  KLSNVTAADT  AVYYCARDPG  QWLVPDAFDI  WGQGTMTSVS
121  S (SEQ ID NO: 37)

```

Nucleotide Sequence of Light Chain Variable Region

```

1  GATATTGTGA  TGAATCAGTC  TCACTCTCC  CTGCCCCTCA  TTCCTGGAGA  GCCGGCCTCC
61  ATCTCCTGCA  GGTCTAGTCA  GAGCCTCCTG  CAGAGTAATG  GAAACAATA  TTTGGATTGG
121  TACCTGCAGA  AGCCAGGGCA  GTCTCCACAG  CTCCTGATCT  ATTTGGGTTC  TAATCGGGCC
181  TCCGGGGTCC  CTGACAGGTT  CAGTGGCAGT  GGATCAGGCA  CAGATTTTAC  ACTGAAAATC
241  AGCAGAGTGG  AGGCTGACGA  TGTGTTGGAT  TATTACTGCA  TGCAAGCTCT  CCAAATTCCT
301  CTCACCTTCG  GCGGAGGGAC  CAAGGTGGAG  ATCAAAC (SEQ ID NO: 40)

```

Amino Acid Sequence of Light Chain Variable Region

```

1  DIVMTQSPLS  LPVIPGEPAS  ISCRSSQSLL  QSNNGNNYLDW  YLQKPGQSPQ  LLIYLGSNRA
61  SGVPDRFSGS  GSGTDFTLKI  SRVEADDVGI  YYCMQALQIP  LTFGGGTKVE  IK
(SEQ ID NO: 38)

```

FIG. 15

		Section 1									
	(1)	1	10	20	30	40	53				
A15-3.10_HC	(1)	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYY									
VH4-59	(1)	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYY									
Consensus	(1)	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYY									
		Section 2									
	(54)	54	60	70	80	90	106				
A15-3.10_HC	(54)	TWNTNYPNPSLKSRVTISVDTSKNQFSLRLSSVTAADTANNYYCARDQGQWLLPD									
VH4-59	(54)	SGSTNYPNPSLKSRVTISVDTSKNQFSLRLSSVTAADTANNYYCAR-----									
Consensus	(54)	S STNYPNPSLKSRVTISVDTSKNQFSLRLSSVTAADTALYYCAR									
		Section 3									
	(107)	107	121								
A15-3.10_HC	(107)	AFDIWGQGTMTVSS									
VH4-59	(98)	-----									
Consensus	(107)	-----									

positives: 79.3%	identity: 76.0%
------------------	-----------------

FIG. 16

Section 1							
	(1)	1	10	20	30	40	53
A15-3.10_LC	(1)	DIQMTQSPSSLSASVGDRTITTCRASQISINYNWYQQKPGKAPKLLIYGASS					
O2	(1)	DIQMTQSPSSLSASVGDRTITTCRASQISINYNWYQQKPGKAPKLLIYGASS					
Consensus	(1)	DIQMTQSPSSLSASVGDRTITTCRASQISINYNWYQQKPGKAPKLLIYGASS					
Section 2							
	(54)	54	60	70	80	90	106
A15-3.10_LC	(54)	LQSGVPSRFSGSGGTDFLTITISLQPEDFATYYCRQSYSTPPECSFGQGTKL					
O2	(54)	LQSGVPSRFSGSGGTDFLTITISLQPEDFATYYCRQSYSTPPECSFGQGTKL					
Consensus	(54)	LQSGVPSRFSGSGGTDFLTITISLQPEDFATYYCRQSYSTPPECSFGQGTKL					
Section 3							
	(107)	107					
A15-3.10_LC	(107)	EIK					
O2	(96)	---					
Consensus	(107)						

positives: 85.3%	identity: 84.4%
------------------	-----------------

FIG. 17

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		Section 1									
		(1)	1	10	20	30	40	53			
A15-3.22_HC	(1)	QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWIRQHPGKGLEWIGFI									
VH4-31	(1)	QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWIRQHPGKGLEWIGFI									
Consensus	(1)	QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGYYWIRQHPGKGLEWIGFI									
		Section 2									
		(54)	54	60	70	80	90	106			
A15-3.22_HC	(54)	YYSGGSTYYNPSSLKSRVTISVDTSKNQFSLKLSSTVTAADTAVYYCAR									
VH4-31	(54)	YYSGGSTYYNPSSLKSRVTISVDTSKNQFSLKLSSTVTAADTAVYYCAR									
Consensus	(54)	YYSGGSTYYNPSSLKSRVTISVDTSKNQFSLKLSSTVTAADTAVYYCAR									
		Section 3									
		(107)	107	117							
A15-3.22_HC	(107)	WGQGTILTVSS									
VH4-31	(100)	-----									
Consensus	(107)	WGQGTILTVSS									

positives: 84.6% identity: 82.9%

FIG. 18

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		Section 1											
		1	10	20	30	40	50						
(1)	(1)	DIQMTQSPSSLSASVGD	RVITITCRASQGI	RNDLGWYQQKPGKAPKRLIYAASS			53						
A15-3.22_LC	(1)	DIQMTQSPSSLSASVGD	RVITITCRASQGI	RNDLGWYQQKPGKAPKRLIYAASS									
A30	(1)	DIQMTQSPSSLSASVGD	RVITITCRASQGI	RNDLGWYQQKPGKAPKRLIYAASS									
Consensus	(1)	DIQMTQSPSSLSASVGD	RVITITCRASQGI	RNDLGWYQQKPGKAPKRLIYAASS									
		Section 2											
		54	60	70	80	90	100						
(54)	(54)	LQSGVPSRFRFSGSGGTEFTLT	ISSLPQPEDE	FATYYICLQHN	SYP	LTFFGGG	TKVEI						
A15-3.22_LC	(54)	LQSGVPSRFRFSGSGGTEFTLT	ISSLPQPEDE	FATYYICLQHN	SYP	LTFFGGG	TKVEI						
A30	(54)	LQSGVPSRFRFSGSGGTEFTLT	ISSLPQPEDE	FATYYICLQHN	SYP	LTFFGGG	TKVEI						
Consensus	(54)	LQSGVPSRFRFSGSGGTEFTLT	ISSLPQPEDE	FATYYICLQHN	SYP	LTFFGGG	TKVEI						
		Section 3											
		(107)	107										
A15-3.22_LC	(107)	K											
A30	(96)	-											
Consensus	(107)												

positives: 88.8% identity: 88.8%

FIG. 19

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Section 1						
	(1)	10	20	30	40	53
A15-3.27_HC	(1)	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYY				
VH4-59	(1)	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYY				
Consensus	(1)	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYY				
Section 2						
	(54)	60	70	80	90	106
A15-3.27_HC	(54)	TWTSNYPNPSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCAR				
VH4-59	(54)	SGSTNYPNPSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCAR				
Consensus	(54)	SSNYPNPSLKSRVTISVDTSKNQFSLRLSSVTAADTAVYYCAR				
Section 3						
	(107)	107	121			
A15-3.27_HC	(107)	AFDIWGQGTMTVSS				
VH4-59	(98)	-----				
Consensus	(107)					

positives: 79.3%	identity: 76.0%
------------------	-----------------

FIG. 20

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		Section 1									
		1	10	20	30	40	53				
A15-3.27_LC	(1)	DIQMTQSPSSLSASVGDRVTITTCRASQGI RNDLGWYQQKPGKAPKRLIYAASS									
A30	(1)	DIQMTQSPSSLSASVGDRVTITTCRASQGI RNDLGWYQQKPGKAPKRLIYAASS									
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITTCRASQGI RNDLGWYQQKPGKAPKRLIYAASS									
		Section 2									
		54	60	70	80	90	106				
A15-3.27_LC	(54)	LQSGVPSRFSGSGGTEFTLTISSLQPEDFATYYC LQHNSYP									
A30	(54)	LQSGVPSRFSGSGGTEFTLTISSLQPEDFATYYC LQHNSYP									
Consensus	(54)	LQSGVPSRFSGSGGTEFTLTISSLQPEDFATYYC LQHNSYP									
		Section 3									
		(107)	107								
A15-3.27_LC	(107)	K									
A30	(96)	-									
Consensus	(107)										

positives: 88.8% identity: 88.8%

FIG. 21

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Section 1									
	1	10	20	30	40	50	53		
A15-3.45_HC	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTF	FSYGF	SWVRQAPGQGLEW	SGWISA				
VH1-18	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTF	TSYGI	SWVRQAPGQGLEW	SGWISA				
Consensus	(1)	QVQLVQSGAEVKKPGASVKVSCKASGYTF	SYG	SWVRQAPGQGLEW	SGWISA				
Section 2									
	54	60	70	80	90	100	106		
A15-3.45_HC	(54)	YNGNTNYAQKLQGRVTMTT	TDST	STAYMELRSLRSD	DDTAVYYCAR	ETKVRGVH			
VH1-18	(54)	YNGNTNYAQKLQGRVTMTT	TDST	STAYMELRSLRSD	DDTAVYYCAR	-----			
Consensus	(54)	YNGNTNYAQKLQGRVTMTT	TDST	STAYMELRSLRSD	DDTAVYYCAR				
Section 3									
	107	123							
A15-3.45_HC	(107)	YYGMDVWGQGT	TVTVSS						
VH1-18	(99)	-----							
Consensus	(107)								

positives: 78.0% identity: 77.2%

FIG. 22

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Section 1									
(1)	1	10	20	30	40	50	60	70	80
A15-3.45_LC	(1)	DIYMTQSPD	SLAVSLGERATI	IICKSSQSS	LYSSNNKNYL	GWYQQKPG	GQPPKLL		
B3	(1)	DIYMTQSPD	SLAVSLGERATI	NCKSSQSS	LYSSNNKNYL	AWYQQKPG	GQPPKLL		
Consensus	(1)	DIYMTQSPD	SLAVSLGERATI	CKSSQSS	LYSSNNKNYL	AWYQQKPG	GQPPKLL		
Section 2									
(54)	54	60	70	80	90	100	110	120	130
A15-3.45_LC	(54)	IYWASTRES	GVPA	RFSGSGGT	DEFTLT	INSLQAED	VAVYCC	QYYS	TPRSFGQ
B3	(54)	IYWASTRES	GVPA	DRFSGSGG	TDEFTLT	INSLQAED	VAVYCC	QYYS	TPRSFGQ
Consensus	(54)	IYWASTRES	GVPA	RFSGSGGT	DEFTLT	INSLQAED	VAVYCC	QYYS	TPRSFGQ
Section 3									
(107)	107	113	119	125	131	137	143	149	155
A15-3.45_LC	(107)	GTMVEIK							
B3	(107)	-----							
Consensus	(107)	GTMVEIK							

positives: 86.7%	identity: 85.0%
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FIG. 23

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Section 1									
(1)	1	10	20	30	40	53			
A15-3.65_HC	(1)	QVQLQESGPGLVKPSQTL	SLTCTVSGGS	INSGG	CYWSWIRQHPGKGL	EWI	GYI		
VH4-31	(1)	QVQLQESGPGLVKPSQTL	SLTCTVSGGS	INSGG	CYWSWIRQHPGKGL	EWI	GYI		
Consensus	(1)	QVQLQESGPGLVKPSQTL	SLTCTVSGGS	INSGG	CYWSWIRQHPGKGL	EWI	GYI		
Section 2									
(54)	54	60	70	80	90	106			
A15-3.65_HC	(54)	YS	SGSTYYNP	SLKSR	IN	SV	DT	SK	NQ
VH4-31	(54)	YS	SGSTYYNP	SLKSR	IN	SV	DT	SK	NQ
Consensus	(54)	YS	SGSTYYNP	SLKSR	IN	SV	DT	SK	NQ
Section 3									
(107)	107	119							
A15-3.65_HC	(107)	DYWGQ	GT	L	V	T	V	S	S
VH4-31	(100)	-----							
Consensus	(107)	-----							

positives: 79.8% identity: 77.3%

FIG. 24

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		Section 1						
	(1)	1	10	20	30	40	53	
A15-3.65_LC	(1)	DIQMTQSPSSLSASVGDRVTITTCQASQDI NNYNWYQQKPGKAPKLLIYDASN						
O8	(1)	DIQMTQSPSSLSASVGDRVTITTCQASQDI SNYNWYQQKPGKAPKLLIYDASN						
Consensus	(1)	DIQMTQSPSSLSASVGDRVTITTCQASQDI NYLNWYQQKPGKAPKLLIYDASN						
		Section 2						
	(54)	54	60	70	80	90	106	
A15-3.65_LC	(54)	LETGVPSRFSGSGGTDFTFTIS GLQPEDIAITYCQQYDTLP LTFGGGTKVEI						
O8	(54)	LETGVPSRFSGSGGTDFTFTIS SLQPEDIAITYCQQYDNL						
Consensus	(54)	LETGVPSRFSGSGGTDFTFTIS LQPEDIAITYCQQYD LP						
		Section 3						
	(107)	107						
A15-3.65_LC	(107)	K						
O8	(96)	-						
Consensus	(107)							

positives: 86.0%	identity: 86.0%
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FIG. 25

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Section 1							
	(1)	1	10	20	30	40	53
A15-6.1_HC	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAVISY					
VH3-30	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAVISY					
Consensus	(1)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSYAMHWVRQAPGKGLEWVAVISY					
Section 2							
	(54)	54	60	70	80	90	106
A15-6.1_HC	(54)	DGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSI					
VH3-30	(54)	DGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR					
Consensus	(54)	DGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR					
Section 3							
	(107)	107	122				
A15-6.1_HC	(107)	YGMDVWGQGTITVTVSS					
VH3-30	(99)	-----					
Consensus	(107)						

positives: 80.3%	identity: 79.5%
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FIG. 26

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Section 1						
	1	10	20	30	40	54
(1)	(1)					
A15-6.1_LC	(1)	DIQMTOSPSLSASVGD	RVTTITCRASQGI	RNYLAWYQQN	PGKVPKLLIY	GSASTL
A20	(1)	DIQMTQSPSSLASVGD	RVTTITCRASQGI	SNYLAWYQQK	PGKVPKLLIY	AASTL
Consensus	(1)	DIQMTQSPSSLASVGD	RVTTITCRASQGI	NYLAWYQQ	PGKVPKLLIY	AASTL
Section 2						
	55	60	70	80	90	107
(55)	(55)					
A15-6.1_LC	(55)	QSGVPSRFSGSGGT	DFTLT	ISSLOPED	VATYYCQKFS	PPFTFGPGTKVDIS
A20	(55)	QSGVPSRFSGSGGT	DFTLT	ISSLOPED	VATYYCQKNN	SAF-----
Consensus	(55)	QSGVPSRFSGSGGT	DFTLT	ISSLOPED	VATYYCQKF	S P

positives: 85.0% identity: 83.2%

FIG. 27

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Section 1						
	1	10	20	30	40	53
A15-6.12_HC	(1)	QVQL	EQSGPGLVKPS	ETLSLTCTVSGGSISSG	TYHWSWIRQHPG	RGLWIGYI
VH4-31	(1)	QVQL	QESGPGLVKPS	QTLSLTCTVSGGSISSG	GYHWSWIRQHPG	RGLWIGYI
Consensus	(1)	QVQL	SGPGLVKPS	TLSLTCTVSGGSISSG	YHWSWIRQHPG	RGLWIGYI
Section 2						
	54	60	70	80	90	106
A15-6.12_HC	(54)	YYSGSTYHNP	SLKSRNTISVDTSKNQFSLKLS	SVTAADTAVYCAR	GGDG	YRY
VH4-31	(54)	YYSGSTYHNP	SLKSRNTISVDTSKNQFSLKLS	SVTAADTAVYCAR	GGDG	YRY
Consensus	(54)	YYSGSTYHNP	SLKSRNTISVDTSKNQFSLKLS	SVTAADTAVYCAR	GGDG	YRY
Section 3						
	107	117				
A15-6.12_HC	(107)	WGQGT	LVTVSS			
VH4-31	(100)	-----				
Consensus	(107)	-----				

positives: 81.2% identity: 77.8%

FIG. 28

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Section 1						
(1)	1	10	20	30	40	53
L2	(1)	EIVMTQSPATLSVSPGERATLSCRASQSSNLLAWYQQKPGQAPRLITNGAST				
A15-6.12_LC	(1)	EIVMTQSPATLSVSPGERATLSCRASQSSNFWAYQQKPGQAPRLITNGAST				
Consensus	(1)	EIVMTQSPATLSVSPGERATLSCRASQSS N AWYQQKPGQAPRLITNGAST				
Section 2						
(54)	54	60	70	80	90	106
L2	(54)	RATGIPAREFSGSGGTEFTLTISSLQSEDFAVYCCQYNNWP				
A15-6.12_LC	(54)	RATGIPAREFSGSGGTEFTLTISSLQSEDFAVYCCQYNNWPRTFGQGTKVEI				
Consensus	(54)	RATGIPAREFSGSGGTEFTLTISSLQSEDFAVYCCQYNNWP				
Section 3						
(107)	<u>107</u>					
L2	(96)	-				
A15-6.12_LC	(107)	K				
Consensus	(107)					

positives: 86.9%	identity: 85.0%
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FIG. 29

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Section 1							
	(1)	1	10	20	30	40	53
A15-6.2_HC	(1)	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYY					
VH4-59	(1)	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYY					
Consensus	(1)	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYY					
Section 2							
	(54)	54	60	70	80	90	106
A15-6.2_HC	(54)	TGNITYNPISLKSRVTNSVDTSKNQFSLKLSVTAADTAVYYCARDPGQWLVPD					
VH4-59	(54)	SGSTINYNPISLKSRVTNSVDTSKNQFSLKLSVTAADTAVYYCAR					
Consensus	(54)	SG T YNPISLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCAR					
Section 3							
	(107)	107	121				
A15-6.2_HC	(107)	AFDIWGQGTMTVSVSS					
VH4-59	(98)	-----					
Consensus	(107)						

positives: 77.7%	identity: 75.2%
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FIG. 30

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		Section 1																									
		1	10	20	30	40	54																				
A15-6.2_LC	(1)	DIVMTQSP LSLPVI PGEPA SISC RSSQSLLQ SNGNNYLDWYLQKPGQSPQLLIY																									
A19	(1)	DIVMTQSP LSLPVT PGEPA SISC RSSQSLLH SNGYNYLDWYLQKPGQSPQLLIY																									
Consensus	(1)	DIVMTQSP LSLPV PGEPA SISC RSSQSLL SNG NYLDWYLQKPGQSPQLLIY																									
		Section 2																									
		55	60	70	80	90	108																				
A15-6.2_LC	(55)	LGSNRASGV PDRFSGSGSGTDFTLKISRVEAD DVGNY YCMQALQIP LTFGGGTK																									
A19	(55)	LGSNRASGV PDRFSGSGSGTDFTLKISRVEAD DVGNY YCMQALQIP LTFGGGTK																									
Consensus	(55)	LGSNRASGV PDRFSGSGSGTDFTLKISRVEAD DVGNY YCMQALQ P																									
		Section 3																									
		(109)	109	112																							
A15-6.2_LC	(109)	VEIK																									
A19	(101)	----																									
Consensus	(109)																										

positives: 85.7%	identity: 83.9%
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FIG. 31

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		Section 1									
		1	10	20	30	40	50	60	70	80	90
A15-6.9_HC	(1)	QVQL	EQSG	PGLV	KPS	ETLS	LTCT	VS	GGSI	SSG	TYHWS
VH4-31	(1)	QVQL	EQSG	PGLV	KPS	ETLS	LTCT	VS	GGSI	SSG	TYHWS
Consensus	(1)	QVQL	EQSG	PGLV	KPS	ETLS	LTCT	VS	GGSI	SSG	TYHWS
A15-6.9_HC	(54)	YYSG	STYH	NP	SLKSR	TTIS	VDTS	KNQF	SLKL	SSVT	AADTA
VH4-31	(54)	YYSG	STYH	NP	SLKSR	TTIS	VDTS	KNQF	SLKL	SSVT	AADTA
Consensus	(54)	YYSG	STYH	NP	SLKSR	TTIS	VDTS	KNQF	SLKL	SSVT	AADTA
A15-6.9_HC	(107)	WGQG	TLVT	VSS							
VH4-31	(107)	WGQG	TLVT	VSS							
Consensus	(107)	WGQG	TLVT	VSS							

positives: 81.2% identity: 77.8%

FIG. 32

positives: 86.9%	identity: 85.0%
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FIG. 33

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Section 1							
	(1)	1	10	20	30	40	53
A15-6.11_HC	(1)	QVQLQESGPGLVKPSQTL	SLTCTVSGGSISSG	THWTWIRQHPGKGLEWIGFI			
VH4-31	(1)	QVQLQESGPGLVKPSQTL	SLTCTVSGGSISSG	YHWSWIRQHPGKGLEWIGFI			
Consensus	(1)	QVQLQESGPGLVKPSQTL	SLTCTVSGGSISSG	YHWSWIRQHPGKGLEWIGFI			
Section 2							
	(54)	54	60	70	80	90	106
A15-6.11_HC	(54)	YYSGSTYYNP	SLKSRVTISVDTSKNQFSLKLS	SVTAADTAVYYCAR	GGDGYKY		
VH4-31	(54)	YYSGSTYYNP	SLKSRVTISVDTSKNQFSLKLS	SVTAADTAVYYCAR	GGDGYKY		
Consensus	(54)	YYSGSTYYNP	SLKSRVTISVDTSKNQFSLKLS	SVTAADTAVYYCAR	GGDGYKY		
Section 3							
	(107)	107	117				
A15-6.11_HC	(107)	WGQGT	LVTVSS				
VH4-31	(100)	-----					
Consensus	(107)	-----					

positives: 83.8%	identity: 82.9%
------------------	-----------------

FIG. 34

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Section 1		1	10	20	30	40	53
A15-6.11_LC L2 Consensus	(1)	1					
	(1)	EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLIIYGAST					
	(1)	EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLIIYGAST					
	(1)	EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQQKPGQAPRLIIYGAST					
Section 2		54	60	70	80	90	106
A15-6.11_LC L2 Consensus	(54)	54					
	(54)	RATGIPARFSGSGGTEFTLTISSLQSEDFAVYCCQYNNWPRTFGQGTKVEI					
	(54)	RATGIPARFSGSGGTEFTLTISSLQSEDFAVYCCQYNNWPRTFGQGTKVEI					
	(54)	RATGIPARFSGSGGTEFTLTISSLQSEDFAVYCCQYNNWPRTFGQGTKVEI					
Section 3		(107)	107				
A15-6.11_LC L2 Consensus	(107)	107					
	(107)	K					
	(96)	-					

positives: 87.9%	identity: 87.9%
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FIG. 35

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Clone #	VH	#del	VH End	#N's	N Sequence	DH	Size of D	D Sequence	#N's	N Sequence	JH	#del	JH Segment
A15-3.10	DP-71/4-59	0	GAGAGA	8	TCAGGGGC	D21-9	8	AGTGGTTA	7	CTACCCG	JH3B	0	ATGCTT
A15-3.22	DP-65/4-31	0	GAGAGA	9	GGGAGATGG	-	-	-	-	-	JH4B	-4	CTTTGA
A15-3.27	DP-71/4-59	0	GAGAGA	8	TCAGGGGC	D21-9	8	AGTGGTTA	7	CTACCCG	JH3B	0	ATGCTT
A15-3.45	DP-14/1-18	0	GAGAGA	6	AACTAA	D3-10	12	GGTTCGGGAGT	2	CC	JH6B	-9	ACTACT
A15-3.65	DP-65/4-31	0	GAGAGA	8	TCGGGAAA	D6-13	8	CAGCTGGT	4	TTTT	JH5A	-11	GA CTAC
A15-6.1	DP-49/3-30	3	GAGAGA	1	T	D3-3	18	CGATTTTGGAGTGGTTA	3	TCG	JH6B	-12	ACTACG
A15-6.2	DP-71/4-59	0	GAGAGA	7	TCCAGGC	D6-19	11	CAGTGGCTGGT	5	CCTG	JH3B	0	ATGCTT
A15-6.9	DP-65/4-31	1	CGAGAG	3	GGG	D5-24	11	GAGATGGCTAC	4	AGAT	JH1	-16	ACTGGG
A15-6.11	DP-65/4-31	1	CGAGAG	3	GGG	D5-24	13	GAGATGGCTACAA	2	GT	JH1	-16	ACTGGG
A15-6.12	DP-65/4-31	1	CGAGAG	3	GGG	D5-24	11	GAGATGGCTAC	4	AGAT	JH1	-16	ACTGGG

Clone #	VK	#del	VH End	#N's	N Sequence	JK	#del	JK end
A15-3.10	02/012/DPK	0	CCCTCC	9	GGAGTGCAG	JK2	-7	TTTTGG
A15-3.22	A30	3	TTACCC	0	0	JK4	0	GCTCAC
A15-3.27	A30	3	TTACCC	0	0	JK1	0	GTGGAC
A15-3.45	B3/DPK24	1	TCCCTC	3	GGT	JK1	-5	CGTTCG
A15-3.65	08/018/DPK	1	TCCCTC	0	0	JK4	-2	TCACTTTC
A15-6.1	A20/DPK4	3	GTCCCC	0	0	JK3	0	ATTCAC
A15-6.2	A3/A19/DPK	1	TTCCTC	0	0	JK4	-2	TCACTTTC
A15-6.9	L2/DPK21	1	GGCCTC	0	0	JK1	-2	GGACGTT
A15-6.11	L2/DPK21	1	GGCCTC	0	0	JK1	-2	GGACGTT
A15-6.12	L2/DPK21	1	GGCCTC	0	0	JK1	-2	GGACGTT

FIG. 36